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# Probe

Newsletter for the USDA Plant Genome Research Program

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## Comparative Mapping Sows Seeds of Progress

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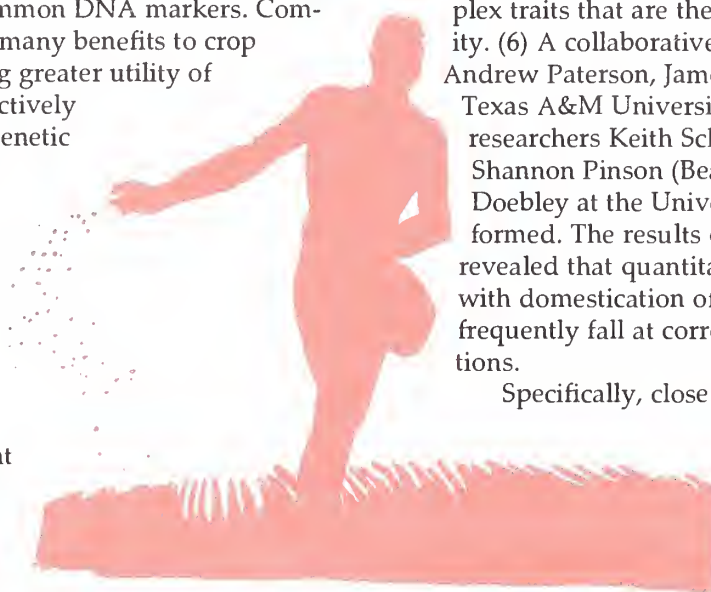
**A**n important component of the USDA Plant Genome Research Program has been comparative mapping, the alignment of the chromosomes of related crop species based on genetic mapping of common DNA markers. Comparative mapping affords many benefits to crop genome analysis, including greater utility of existing DNA probes, effectively increasing the density of genetic markers in many species simultaneously. In addition, comparative mapping offers new opportunities for investigating plant evolution.

Detailed comparative maps are being assembled for several plant families, such as the (1) *Solanaceae*, (2) *Poaceae*, *Fabaceae* (N. D. Young, pers. comm.), (3) *Brassicaceae*, and (4) *Malvaceae*, which include many of the crops that feed and clothe humankind. (5) In one particularly well-studied plant family, the *Poaceae*, extensive conservation of gene repertoire and gene order along the chromosomes has led to the suggestion that the cultivated cereals might be treated as essentially a single genetic system.

### Comparative mapping of quantitative trait loci

Recent results suggest that comparative mapping may have even greater utility than previously envisioned, reaching directly into the molecular dissection of complex traits that are the basis of agricultural productivity. (6) A collaborative research project involving Andrew Paterson, James Stansel, and James Irvine at Texas A&M University, together with USDA-ARS researchers Keith Schertz (College Station, Texas), Shannon Pinson (Beaumont, Texas), and John Doebley at the University of Minnesota was formed. The results of this collaborative effort revealed that quantitative trait loci (QTL) associated with domestication of sorghum, rice, and maize frequently fall at corresponding genetic map locations.

Specifically, close correspondence appears to occur among QTL affecting traits such as seed size; shattering of the inflorescence; and short-day flowering of sorghum, sugarcane, maize, and rice. This correspondence is mirrored by (7) a companion study in which 185 genes and QTL reported by many independent investigators to affect height and flowering of maize and other species were collated with each other and with a new map of the genes associated with height and flowering in sorghum. (8) An independent study of a smaller set of QTL in maize and sorghum reinforces



this theme of correspondence. While correspondence of QTL in different species of the plant genera (9) *Lycopersicon* and (10) *Vigna* had previously been reported, such correspondence spans relatively short periods of genetic divergence, and in fact the relative promiscuity of plant species makes it difficult to preclude the possibility of recent gene flow.

Correspondence between QTL has been suggested, not only between different taxa, but also between duplicated chromosome segments within a particular species, indicating that chromosome duplication may contribute to polygenic inheritance. Specifically, (6) pairs of loci affecting shattering of the maize inflorescence, (7) maize height and flowering, and sorghum height, fall on chromosome segments that appear to correspond, based on genetic mapping of duplicated DNA markers. While only a subset of QTL appear to be associated with chromosome duplication, it is offered as one of many mechanisms by which quantitative traits might evolve.

## Implications of corresponding QTL for life sciences research

The suggestion that mutations in corresponding genes may account for phenotypic variation in species such as sorghum, maize, and rice, reproductively isolated for an estimated 65 million years, has widespread implications. Perhaps first and foremost, QTL analysis in one taxon may be predictive of results in other taxa. Such predictive value would afford broader utility of QTL mapping results than was previously envisioned, enabling research on easy systems to be extrapolated to more difficult

systems, and minimizing redundancy.

For example, recent results describe a set of QTL largely responsible for rhizomatousness of johnsongrass, one of the world's most important agricultural weeds (11). Such research is difficult to conduct, as rhizomes grow underground, and are very laborious to measure accurately. Rhizomatous forms of both sugarcane and rice harbor genes of potential value to agriculture but cannot be grown in the United States for fear of introducing new weed species to these crops.

Comparative mapping may afford the means to breed rhizomatousness out of these weedy relatives, affording safe access to valuable genes held in these exotic gene pools. On the flip side, aggressive rhizomes contrib-

ute to productivity of many forage and turf grasses, essential to the U.S. agroecosystem both for animal fodder and in erosion control. Research in progress seeks to determine whether growth enhancement of several forage and turf species may derive from use of DNA markers closely linked to rhizomatousness in sorghum.

Correspondence of QTL across diverse taxa also provides a strong empirical foundation in support of model systems research on complex phenotypes. For example, the ease of genetic analysis possible in rodents and agricultural mammals has permitted mapping of genes associated with diabetes, hypertension, obesity, alcohol/drug addiction, and other medically important phenotypes. The inherent difficulties associated with mapping complex traits in humans are partly amelio-

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rated by the possibility of cloning QTL in mouse (for example) that account for phenotypic variation in humans. In a like manner, crop plants that grow particular plant organs of extraordinary size, such as the enlarged root of turnip, inflorescence (curd) of cauliflower, or fruit of tomato, might be used to identify developmentally important genes in which genetic variants impair survival or reproduction in other species.

## Maximizing the value of future genome mapping results

Many investigators are enhancing the value of their results to the scientific community by making an extra effort to facilitate comparative analysis. There is growing awareness that once a gene has been mapped by any of a wide range of DNA-based techniques now available, it is important that the diagnostic marker(s) be linked to a comprehensive genetic map (or previously mapped DNA clones) that affords integration with related taxa. Genetic maps based on conserved DNA sequences are becoming increasingly prevalent, mapped DNA markers are widely available, and few, if any, genetic mapping labs can resist the opportunity to "put one more marker on the map," especially one linked to an important phenotype. By using the fortuitous tools that nature offers us for comparative analysis of plant chromosomes, an ever larger and more complex body of genetic data on major crops can be integrated into a more coherent and therefore more useful information base, valuable for improving the long-term productivity and sustainability of U.S. agriculture.

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## Competitive Edge



# Report on the 1995 Plant Genome Awards

**I**n 1995, the National Research Initiative Competitive Grants Program (NRICGP) made available \$9,507,886 for plant genome research, out of which 68 grants were awarded. The Plants Division of the NRICGP in USDA's Cooperative State Research, Education, and Extension Service administered the grants.

The total grant amount is lower than in previous years, as is the number of awards given, largely because of Federal budget reductions. Despite these developments, the average amount per award and average number of years per award have increased from previous years, thus increasing the award's value to recipients (see table 1).

To be considered for the awards, scientists from the research community submitted mission-oriented proposals that addressed the goal of improving agronomic qualities of plants through genomic research.

Ed Kaleikau, acting division director of the Plants Division, and Steve Tanksley, panel manager, of the Plant Breeding and Biometry Department, Cornell University, selected peer panel members and ad hoc reviewers for the proposals in concurrence with the NRI Chief Scientist and USDA administration. The panel considered and discussed all the reviews, then ranked the proposals based on scientific merit, relevance to agriculture, and quality of research facilities and personnel.

Award recipients represented 37 research institutions (see next page) studying 30 species (see next page for number of awards per species and dollar amounts). According to Ed Kaleikau, comparative mapping and map-based cloning were hot topics among researchers across the board. He added that this trend underscores the importance of the Plant Genome Database, which centralizes such information for researchers to use.

The data for the tables was supplied by the NRICGP staff, and compiled into tables by Dr. Garry Smith, USDA-ARS, Fargo, North Dakota. ♦

**Table 1**

### NRI PLANT GENOME REVIEWED AWARDS 1991-95

Year	Awards	\$ Amount	Avg Years Per Award	Average \$ Per Award	Percent Success Rate
1991	76	10,489,525	2.2	138,020	30
1992	95	12,191,822	2.1	128,335	34
1993	91	12,126,238	2.3	133,255	34
1994	104	11,730,074	2.0	112,876	33
1995	68	9,507,886	2.5	139,822	27
Totals/avg.	434	56,054,545	2.2	130,462	32

## Institutions Receiving NRI Plant Genome Awards 1995

Auburn  
Cal Berkeley  
Cal Davis  
Cal Riverside  
Cal San Diego  
Case Western  
Clemson  
Cold Spring Harbor  
Colorado State  
Cornell  
Florida  
Illinois  
Indiana  
Iowa State  
Kansas State  
Kentucky  
Louisiana State  
Maine  
Minnesota  
Missouri  
Montana State  
Nebraska  
North Carolina  
North Carolina State  
North Dakota  
North Dakota State  
Oregon State  
Purdue  
Rhode Island  
Southern Mississippi  
Texas A&M  
USDA/ARS, PGEC  
USDA/ARS  
USDA Forest Service  
V. Commonwealth  
Washington  
Wisconsin

## Species Represented by Plant Genome Awards 1995

Species	No. of Awards	Amount	Percent of Total
Agrobacterium	1	\$100,000	1.1
Alfalfa	1	\$50,000	0.6
<i>Arabidopsis</i>	7	\$1,121,000	11.8
Barley	2	\$440,000	4.6
Bean	3	\$302,725	3.2
<i>Brassica</i>	3	\$535,000	5.6
Chokecherry	1	\$50,000	0.5
Citrus	1	\$185,000	1.9
Cotton	1	\$49,947	0.5
<i>E. coli</i>	1	\$100,000	1.1
Lettuce	1	\$410,000	4.3
Loblolly pine	2	\$325,143	3.4
Maize	18	\$2,182,000	22.9
Millet	2	\$245,000	2.6
Pea	1	\$120,000	1.3
Peach	1	\$250,000	2.6
Peanut	1	\$100,000	1.1
Pearl millet	1	\$105,000	1.1
Petunia	1	\$115,000	1.2
Pine	1	\$210,000	2.2
Populus	1	\$175,000	1.8
Rice	4	\$686,000	7.2
Sorghum	2	\$286,000	3.0
Soybean	3	\$393,000	4.1
Spring wheat	1	\$50,000	0.5
Sunflower	1	\$320,000	3.4
Sweet potato	1	\$49,476	0.5
Tobacco	7	\$975,000	10.3
Tomato	5	\$920,000	9.7
Wheat	4	\$350,000	3.7
<b>Totals</b>	<b>*68</b>	<b>*\$9,507,886</b>	<b>*100.0</b>

\*Column totals do not reflect sum of column numbers because some awards involve more than one species.

Turn the page for listing of  
1995 Award Recipients



## USDA National Research Initiative Competitive Grants Program Plant Genome Grants—Fiscal Year 1995

Henry V. Amerson, David M. O'Malley, Ronald R. Sederoff  
Role of Major Genes for Resistance in the Loblolly Pine-Fusiform Rust Forest Pathosystem  
North Carolina State University

Barbara Joan Baker  
Isolation of the TMV Resistance Gene, *N'*  
Plant Gene Expression Center, USDA/ARS

Patricia A. Bedinger  
Analysis and Cloning of Male Sterility Genes  
Colorado State University

Jeffrey L. Bennetzen  
Multi-Institutional Research Coordination Group on  
Integration of Grass Genome Studies  
Purdue University

James A. Birchler  
Molecular Analysis of Maize Centromeres  
University of Missouri

Frederick A. Bliss  
Molecular Tagging Genes for Nematode Resistance and  
Tree Growth in Peach  
University of California, Davis

Harvey D. Bradshaw, Jr.  
Mapping Quantitative Trait Loci in *Populus*  
University of Washington

Gordon C. Cannon  
Nucleoid Protein Composition and Phosphorylation  
During Plastid Development in Soybean  
University of Southern Mississippi

Vicki L. Chandler  
1995 Gordon Research Conference on Epigenetic Effects  
on Gene Expression  
University of Oregon

Christine D. Chase  
Mitochondrial-Nuclear Interactions in S Male-Sterile  
Maize  
University of Florida

Zong Ming Cheng  
Host/Pathogen Interactions and Inheritance of XMLO  
Resistance in Chokecherry  
North Dakota State University

Jeffrey L. Dangl  
Molecular Genetics of Downy Mildew Resistance: The  
*Arabidopsis Rpp8* Cluster  
University of North Carolina

William O. Dawson  
Plant Resistance and Recognition of Tobamoviruses  
University of Florida

Ismail Dweikat, Herbert W. Ohm  
Detection of Hessian Fly Resistance Genes in Wheat  
Purdue University

William B. Eggleston  
Origin and Interactions of a Naturally Occurring,  
Tandem Duplication in Maize  
Virginia Commonwealth University

Elias M. Elias  
Molecular Mapping of High Grain Protein Content in  
Durum Wheat  
North Dakota State University

Stephen K. Farrand  
CIS- and Trans-Acting Functions Mediating Ti Plasmid  
Transfer  
University of Illinois at Urbana-Champaign

Daniel R. Gallie  
Isolation of RNA-Binding Proteins Involved in  
Regulating Translation  
University of California, Riverside

Stanton B. Gelvin  
Early Events in T-DNA Transcription and Integration  
Purdue University

J.J. Giovannoni  
High Density Mapping and Isolation of Genes  
Regulating Tomato Fruit Ripening  
Texas A&M University

Peter Goldsbrough, Gebisa Ejeta  
Drought Tolerance in Sorghum: Mapping of QTLs and  
Analysis of Near-Isogenic Lines  
Purdue University

Carol M. Hamilton  
Evaluation and Application of a New BAC Library  
Vector Designed for Transfer of Large DNA Inserts to  
Cornell University

Larkin Curtis Hannah  
Intron-Enhanced Gene Expression in Maize  
University of Florida

Thomas K. Hodges, Leszek A. Lyznik  
Homologous and Site-Specific DNA Recombination for  
Genomic Modifications of Plants  
Purdue University

Scot H. Hulbert  
An Analysis of the *Rpl* and *Rp3* Loci of Maize  
Kansas State University

Arthur Garfield Hunt  
Characterization of a Plant Poly(A) Polymerase  
University of Kentucky

Roger William Innes  
Use of *Arabidopsis* DNA Markers To Isolate a Disease  
Resistance Gene From Soybean  
Indiana University

Richard A. Jorgensen  
Co-Suppression, Paramutation and Transgene-Elicited  
Pigmentation Patterns  
University of California, Davis

Shawn Michael Kaeppler, K. Arumuganathan, Heidi  
Flewelling Kaeppler  
Chromosome Specific Libraries for Maize Genome  
Research  
University of Nebraska-Lincoln

Harry John Klee  
Modulation of Ethylene Sensitivity in Tomato  
University of Florida

Steven J. Knapp  
A Genetic Map and Mapping Resources for Sunflower  
(*Helianthus annuus. L.*)  
Oregon State University

Sondra G. Lazarowitz  
Molecular Genetics of Geminiviruses Pathogenesis  
University of Illinois

Peggy G. Lemaux  
Targeted Gene Tagging by Generating Barley With  
Maize Ds at Defined Locations  
University of California, Berkeley

Yi Li  
High Performance Liquid Chromatography for Plant  
Molecular Research  
Kansas State University

George H. Liang, Daniel Z. Skinner  
Biostic Gametophyte Transformation of Alfalfa  
Kansas State University

Din-Pow Ma  
Characterization of Cotton Fiber Genes and Their  
Regulatory Elements  
Mississippi State University

John Munson Martin  
Predicting Progeny Variation from Parental Diversity in  
Spring Wheat  
Montana State University

Future updates posted at URL:  
<http://www.nal.usda.gov/pgdic>

Phillip E. McClean  
Fine Structure Mapping of Disease Resistance Related  
Genes in Common Bean  
North Dakota State University

William Richard McCombie, Robert Martiensson  
Structural and Functional Analysis of a Region of the  
*Arabidopsis* Genome  
Cold Spring Harbor Laboratory

Michael D. McMullen, Patrick F. Byrne, Maurice E.  
Snook, Neil W. Widstrom  
Genetic Control of Corn Earworm Resistance Factors  
in Maize  
University of Missouri

Richard W. Michelmore  
Structure and Variation of Resistance Gene Complexes  
in Lettuce  
University of California, Davis

Gloria A. Moore, Frederick G. Gmitter  
Genetic Transformation of Mature Meristematic Tissue  
in Perennial Plants  
University of Florida

Walter C. Mueller, Eric M. Roberts, Carl H. Beckman  
Mechanisms of Polygene Resistance in Tomato Plants  
Infected With *Fusarium*  
University of Rhode Island

Norimoto Murai  
Methionine Enhancement of the Bean Seed Storage  
Protein Phaseolin = Plant Expression Assay  
Louisiana State University

June B. Nasrallah, Mikhail E. Nasrallah  
A Structural and Transcriptional Analysis of the S-Locus  
Region of *Brassica*  
Cornell University

Kathleen J. Newton  
Transcriptional Regulation in *Zea* Mitochondria  
University of Missouri

Brent L. Nielsen  
Detailed Characterization of Tobacco Chloroplast DNA  
Replication Initiation Sites  
Auburn University

Basil J. Nikolau, Patrick S. Schnable  
Molecular Analysis of Meiotic Recombination  
Iowa State University

Thomas C. Osborn  
Defining Genes for Vernalization Requirement in  
*Brassica*  
University of Wisconsin

Peggy Ozias-Akins, Wayne W. Hanna  
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University of Georgia

Calvin O. Qualset  
Research Collaboration Group on Molecular Mapping in  
Wheat and Its Relatives  
University of California, Davis

Sriyani Rajapakse, Janice R. Bohac  
Molecular Analysis of *Beta-amylase* Gene in Sweet potato  
and Wild *Ipomoea* Species  
Clemson University

Pamela C. Ronald  
Positional Cloning of a Major Gene From a Durably  
Resistant Rice Cultivar  
University of California, Davis

Robert J. Schmidt, Martin F. Yanofsky  
An Analysis of Floral Regulatory Genes in Maize  
University of California, San Diego

Mitchell M. Sewell, David E. Harry, David B. Neale  
Comparative Mapping in the Genus *Pinus*  
Institute of Forest Genetics/Pacific Southwest Research  
Station

William F. Sheridan, Inna N. Golubovskaya, Yasuo  
Hotta  
Maize Desynaptic Mutants: Chromosome Pairing,  
Synapsis and Recombination Nodules  
University of North Dakota

Stephen M. Stack, Nora L.V. Lapitan  
Physical Mapping of Genes and RFLP Markers on  
Tomato Pachytene Chromosomes  
Colorado State University

James L. Starr, M. Burow, A.H. Paterson, C.E. Simpson  
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Resistance in Peanut-Utility in Gene Management  
Texas A&M University

Thomas Dermot Sullivan  
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Bruce S. Weir  
Quantitative Genetics Gordon Conference  
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Susan Mary Wick  
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University of Minnesota

Roger Philip Wise, Richard Anthony DeScenzo  
Genetic and Physical Analysis of the *Mla* Resistance  
Gene Cluster in Barley  
Iowa State University-USDA / ARS

Ray J. Wu  
Isolation of Megabase-Sized DNA and Construction of  
Physical Maps in *Arabidopsis* and Rice  
Cornell University

Eve S. Wurtele, James T. Colbert  
Evaluation of *zrp4* a Gene Expressed in Endodermal  
Cells of Roots During Suberin Deposition  
Iowa State University

Nevin D. Young, James H. Orf, David A. Somers  
High Resolution Mapping and Positional Cloning Tools  
To Study Soybean Cyst Nematode Resistance  
University of Minnesota ◆

## Interagency Program: *Arabidopsis thaliana* Genome Sequencing Project

The National Science Foundation (NSF), Department of Energy (DOE), and USDA have solicited proposals from a broad community of scientists to initiate systematic sequencing of the genome *Arabidopsis thaliana*. The ultimate goal of the joint program is to sequence the entire *Arabidopsis* genome by the year 2004 or before.

The program anticipates supporting up to three 3-year awards, through cooperative agreements or grants. The exact amount will depend on the advice of reviewers and on the availability of funds, with the cost shared by the participating Federal agencies. Applications were due by January 16, 1996.

The Multinational Coordinated *Arabidopsis thaliana* Genome Research Project was established in 1990 to develop *Arabidopsis thaliana* as an experimental model system for studies of flowering plants. Since that time, rapid scientific advances in *Arabidopsis* research, coupled with progress in large-scale genome sequencing of several genomes from other model organisms, has led researchers to estimate that sequencing of the entire

genome could take place by 2004, based on the current genome sequencing technology and the available resources (North American *Arabidopsis* Steering Committee Workshop Report, NSF95-43, pp. 35-39). The time frame is expected to be reduced substantially as the relevant technologies are further developed.

To maximize efficient use of available resources and minimize duplication of effort, the joint NSF/DOE/USDA project will be coordinated with other ongoing genome projects, including the National Institutes of Health's Human Genome Research Project and the USDA Plant Genome Research Program, as well as with other national and transnational programs around the world.

A complete text of the program announcement may be obtained by calling or writing PGDIC or on the World Wide Web, at:  
[http://www.nal.usda.gov/answers/info\\_centers/pgdic/pgdic.html](http://www.nal.usda.gov/answers/info_centers/pgdic/pgdic.html). ◆

Touching Base with Edie Paul



## New Release of the RiceGenes Database

Edie Paul, Database Curator  
Department of Plant Science  
Cornell University  
Ithaca, NY



**A** new release of the RiceGenes database is now available as Version 3.0.3. This version is based on the ACEDB Version 3.0 software. The next release will include a migration to ACEDB Version 4.0.

The major new category of information contained in this release is a maize map based on over 700 rice, oat, barley, and maize markers. It is an expanded version of the comparative rice-maize map published by Ahn and Tanksley in 1993. The comparative information is stored in two new classes, *Chrom\_Block* (the maize components) and *Homoeology* (the rice

components). We used several special genetic map display mechanisms to present this information.

If you are using the ACEDB interface, you can easily access the data by clicking on the chromosomal region of interest. A window with a description of the interval should then appear. It might help to know that the naming convention we adopted, M8-R1-n (or R1-M8-n), describes a segment in common between maize chromosome 8 and rice chromosome 1. The last digit is just a numerical designation to keep things unique. The maize map and the raw mapping data it is based on are also available as files to download from the RiceGenes gopher.

For World Wide Web users, we have incorporated hot links from the RiceGenes database into MaizeDB for locus and probe records. This will give you access to the most up-to-date version of the maize information. We also have hot links into Germplasm Resources Information Network from various germplasm records and into the public sequence databases for sequence information.

Volumes 1-9 of the Rice Genetics Newsletter (RGN) are now available in their entirety over gopher and WWW. These summarize much historical genetic information on rice that cannot easily be

found elsewhere. If your searches of the RiceGenes database don't return any hits, I would strongly recommend searching the RGN's. The gopher and WWW also include the new maize/rice comparative information.

The UNIX version of the database is available as a compressed .tar file via anonymous ftp from the site: [probe.nal.usda.gov](ftp://probe.nal.usda.gov/pub/rice/ricegenes3.0.3.tar.Z), directory pub/rice, file [ricegenes3.0.3.tar.Z](#). Be sure to get the README.rice file as well.

The RiceGenes Gopher runs on: [nightshade.cit.cornell.edu](http://nightshade.cit.cornell.edu) port 70



## Touching Base with Phillip McClean



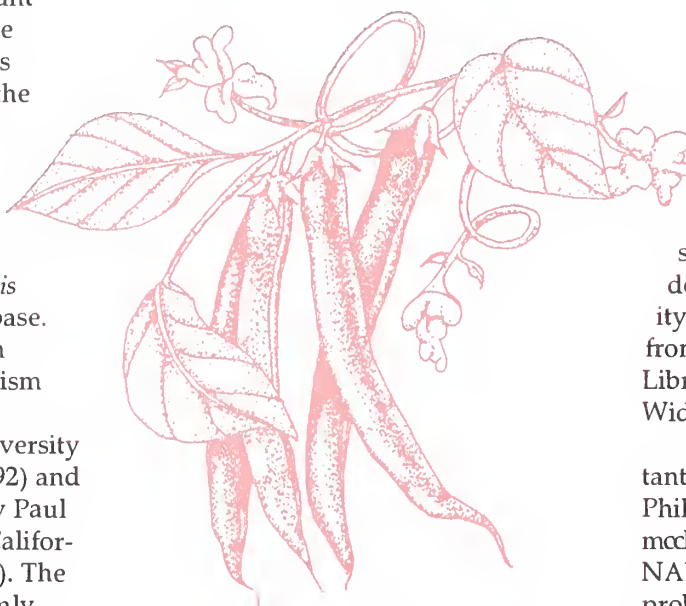
# BeanGenes

Phillip E. McClean, Database Curator  
Department of Plant Sciences  
North Dakota State University  
Fargo, North Dakota

BeanGenes is a database containing information about *Phaseolus* and *Vigna* spp. It is part of the legume database effort coordinated by Randy Shoemaker, USDA/ARS (SoyBase) and is funded by the USDA Plant Genome Project. Phil McClean, Department of Plant Sciences, North Dakota State University, is the BeanGenes curator. The database uses the ACeDB software for data storage and organization.

BeanGenes contains several classes of information. All the published molecular maps of *P. vulgaris* are represented in the database. These include the restriction fragment length polymorphism (RFLP) map developed by Eduardo Vallejos at the University of Florida (Vallejos et al. 1992) and the RFLP map developed by Paul Gepts at the University of California, Davis (Gepts et al. 1993). The combined RFLP and randomly amplified polymorphic DNA (RAPD) map developed by Michel Dron at the University of Paris, Sud can also be accessed. Nevin Young of the University of Minnesota has provided RFLP maps of mung bean (*Vigna radiata*) and cowpea (*V. unguiculata*).

Associated with each molecular map are loci and probe information. The loci information describes the probes or RAPD's used to define the locus, and the probe data provide specific information about a given probe.



BeanGenes also contains all the gene information compiled by Mark Bassett at the University of Florida (Bassett 1993). All published references to the genes are also included.

The colleague list on BeanGenes contains the list of individuals and organizations

actively involved in bean research. Howard Schwartz (Colorado State University) maintains the list for the Bean Improvement Cooperative.

The major and minor diseases of the *Phaseolus* and *Vigna* spp. are described in BeanGenes. CIAT provided images for many of the *Phaseolus* diseases.

The database can be accessed from the BeanGenes server. Requirements include the following: X-Windows capability, knowledge of the ACeDB software, and a login ID. If you do not have X-Windows capability, you can access BeanGenes from the National Agricultural Library using either the World Wide Web or Gopher.

The following are the important electronic addresses:  
Phil McClean - e-mail: [mclean@beangen.es.cws.ndsu.nodak.edu](mailto:mclean@beangen.es.cws.ndsu.nodak.edu)  
NAL WWW Server: <http://probe.nal.usda.gov:8300//plant/index.html>  
NAL Gopher Server: [probe.nal.usda.gov](http://probe.nal.usda.gov) ♦

Mention of a trade name or brand does not constitute endorsement or recommendation by the U.S. Department over similar products not named.

## Other Pursuits



# Organelle Genomics

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Montreal (Quebec), CANADA

## Symbioses

Mutually beneficial symbiotic relationships are common in biology, in both nature and the scientific process. Symbiotic events have characterized the evolution of eukaryotes (Gray 1992) as cells joined forces to create new, more successful forms. Indeed, the present day plant genome is a composite of at least two such (endosymbiotic) events, resulting in three distinct genomes within the cell (plastid, mitochondrion and nucleus; fig. 1).

The origins and information content of organelle genomes is being dissected by an alliance of Canadian research groups, which has brought together individuals with a diversity of expertise. Two separate endeavors, an organelle genome sequencing program and an organelle database project, are cooperating to create a focus of organelle genomics (fig. 1).

## OGMP—an organelle genome program

The OGMP (Organelle Genome Megasequencing Program) is a

collaborative effort of Canadian research groups with expertise in genomics, evolution, mathematics, and informatics, united under the umbrella of the CIAR (Canadian Institute for Advanced Research) Program in Evolutionary Biology (table 1). The multidisciplinary approach of the OGMP is an essential component of any genomics program, where the generation and management of large quantities of data requires broad and deep skills across the fields of biology and computer science.

The goal of the OGMP since its inception in 1992 has been to

**Table 1.** Members of the OGMP (Organelle Genome Megasequencing Program) and GOBASE (Organelle Genome Database Project)

<u>Individual</u>	<u>Affiliation</u>	<u>Institution</u>	<u>Contact</u>
Gertraud Burger	OGMP Unit/GOBASE	University of Montreal	burgerg@bch.umontreal.ca
Robert Cedergren	OGMP Team	University of Montreal	ceder@bch.umontreal.ca
Brain Golding	OGMP Team	McMaster University	brian@evol.biology.mcmaster.ca
Micheal W. Gray	OGMP Unit/GOBASE	Halifax University	mgray@ac.dal.ca
Maria Korab-Laskowska	GOBASE	University of Montreal	korablam@bch.umontreal.ca
B. Franz Lang	OGMP Unit/GOBASE	University of Montreal	langf@bch.umontreal.ca
Claude Lemieux	OGMP Team	University of Laval	2020014@saphir.ulaval.ca
Timothy G. Littlejohn	OGMP Unit ID/GOBASE	University of Montreal	tim@bch.umontreal.ca
Isabelle Plante	OGMP Unit	University of Montreal	plantei@bch.umontreal.ca
Peirre A. Rioux	OGMP Unit ID/GOBASE	University of Montreal	riouxp@bch.umontreal.ca
Daine Saint-Louis	OGMP Unit	University of Montreal	saintd@bch.umontreal.ca
David Sankoff	OGMP Team	University of Montreal	sankoff@ere.umontreal.ca
Monique Turmel	OGMP Team	University of Laval	2020141@saphir.ulaval.ca
'un Zhu	OGMP Unit	University of Montreal	zhuy@bch.umontreal.ca

Members of the Informatics Division (ID) of the OGMP Unit are indicated, with the rest belonging to the Molecular Biology Division (MBD). Further information on the OGMP Unit can be obtained from Gertraud Burger, on Informatics from Tim Littlejohn and on the OGMP and GOBASE projects from their coordinator, B. Franz Lang.

**Table 2.** Organellar genomes sequenced by OGMP

<u>Organism</u>	<u>Classification</u>	<u>Size (kb)</u> <u>mtDNA</u>	<u>Sequenced</u> <u>mtDNA</u>	<u>Sequenced</u> <u>ptDNA(kb)</u>	<u>Reference</u>
<i>Prototheca wickerhamii</i>	Chlorophyte	55.3	100%	10.2	Wolff et al. 1993a,b;1994
<i>Tetraselmis maculata</i>	Chlorophyte	50	12%	15.9	-
<i>Pedinomonas minor</i>	Chlorophyte	23	28%	0.4	-
<i>Ulva lactuca</i>	Chlorophyte	?	0%	6.4	-
<i>Rhodomonas salina</i>	Chlorophyte	47	95%	34.2	-
<i>Ochromonas danica</i>	Chlorophyte	41.1	100%	11.2	In preparation
<i>Porphyra purpurea</i>	Rhodophyte	36.6	100%	5.8	Submitted
<i>Acanthamoeba castellanii</i>	Rhizopod	41.6	100%	-	Burger et al. 1995
<i>Tetrahymena pyriformis</i>	Ciliate	47.3	100%	-	In preparation
<i>Cafeteria roenbergensis</i>	Bicosoecid	43.4	100%	-	In preparation
<i>Reclinomonas americana</i>	Histionid	65	92%	-	-
<i>Malawimonas</i> sp.	Histionid	40	23%	-	-

Organelle genomes sequenced or being sequenced by the OGMP Unit, mtDNA- mitochondrial DNA; ptDNA- plastid DNA.

generate a phylogenetically diverse collection of organelle genome sequences to delve into the mode and tempo of organelle genome evolution. The OGMP is generating a quantity of data that should permit assessment of how (and the number of times) plastids and mitochondria arose, how their genomes have changed, and what accounts for the different evolutionary patterns they display. One focus of the OGMP has been to resolve the phylogenetic relationships between the major protist phyla such as ciliates, rhodophytes, cryptophytes, stramenopiles, and rhizopods. Another emphasis has been to investigate the base of the evolutionary bifurcation between the green lineages of the charophytes/embryophytes and the chlorophytes. These questions, which have proven to be intractable with single gene sequences, have been resolved using the large data sets of complete mitochondrial sequences (over 475 kb of new organelle sequences so far--table 2; OGMP, in preparation).

The OGMP is structured into two components, the Team and the Sequencing Unit that work together for mutual benefit. (fig. 1). The

Team, composed of the seven collaborating research groups, decides on the overall directions of the program and provides the raw material (purified organellar DNA) to the Unit. The Unit then clones and sequences the supplied DNA, manages the production of the complete genome sequence, and performs analysis of gene content and organization. Completed genome sequences are further analyzed in collaboration with the Team, which continues analysis (for examples, phylogenetics) and uses this information to guide the selection of additional key genomes to be sequenced and the planning of spin-off projects (for example, the modes of mitochondrial gene expression).

The Sequencing Unit is further divided into two components: the Molecular Biology Division (MBD) and the Informatics Division (ID). The Molecular Biology Division is charged with performing all the molecular biology within the Unit as well as with the overall project management and analysis. The Informatics Division's mission is to support the Molecular Biology Division for all their computing

requirements (software, hardware, databases, networks) and to conduct bioinformatics research. The large quantity of data generated by the OGMP necessitates that nearly 45 percent of its resources be channeled into informatics, which has proven to be pivotal for data management, analysis, and decision support (Burger et al., in preparation).

## GOBASE--an integrated database for organelle genomics

As a new initiative, the goal of the GOBASE project is to construct an organelle genome database, integrating all the information generated by the OGMP and other organelle genome research groups. The GOBASE database will:

- serve as an integrated, centralized repository for all organelle information
- include data from nucleic acid and protein sequences, polymorphisms, and genetic and physical maps to biochemical and physiological data
- model organelle RNA secondary structures

- facilitate organelle data submission from the community
- develop novel approaches to database integration and genomic data analysis

GOBASE will provide a framework for the access to, and analysis of, organelle data, including: comparative genomics, molecular biology, evolutionary biology, population genetics, and biogenesis. The GOBASE project invites comments and suggestions for its development from the community (see table 1 for contact information).

## Future and further information

Genomics is unquestionably one of the most exciting movements in biology today, and organelle genomes continue to provide the most exhaustive set of completely sequenced cellular genomes (with over 50 complete sequences presently available in GenBank and growing by more than 3 genomes per year by the OGMP effort alone; Littlejohn 1994). The Canadian Organelle Genomics group will continue to rely on

multidisciplinary, symbiotic relationships for its progress, linking expertise in organismal biology, molecular biology, evolution, and informatics. A dataset of this size permits comparative studies that reveal much about genome structure, function and evolution.

Further information on the projects can be obtained at the following World Wide Web sites:

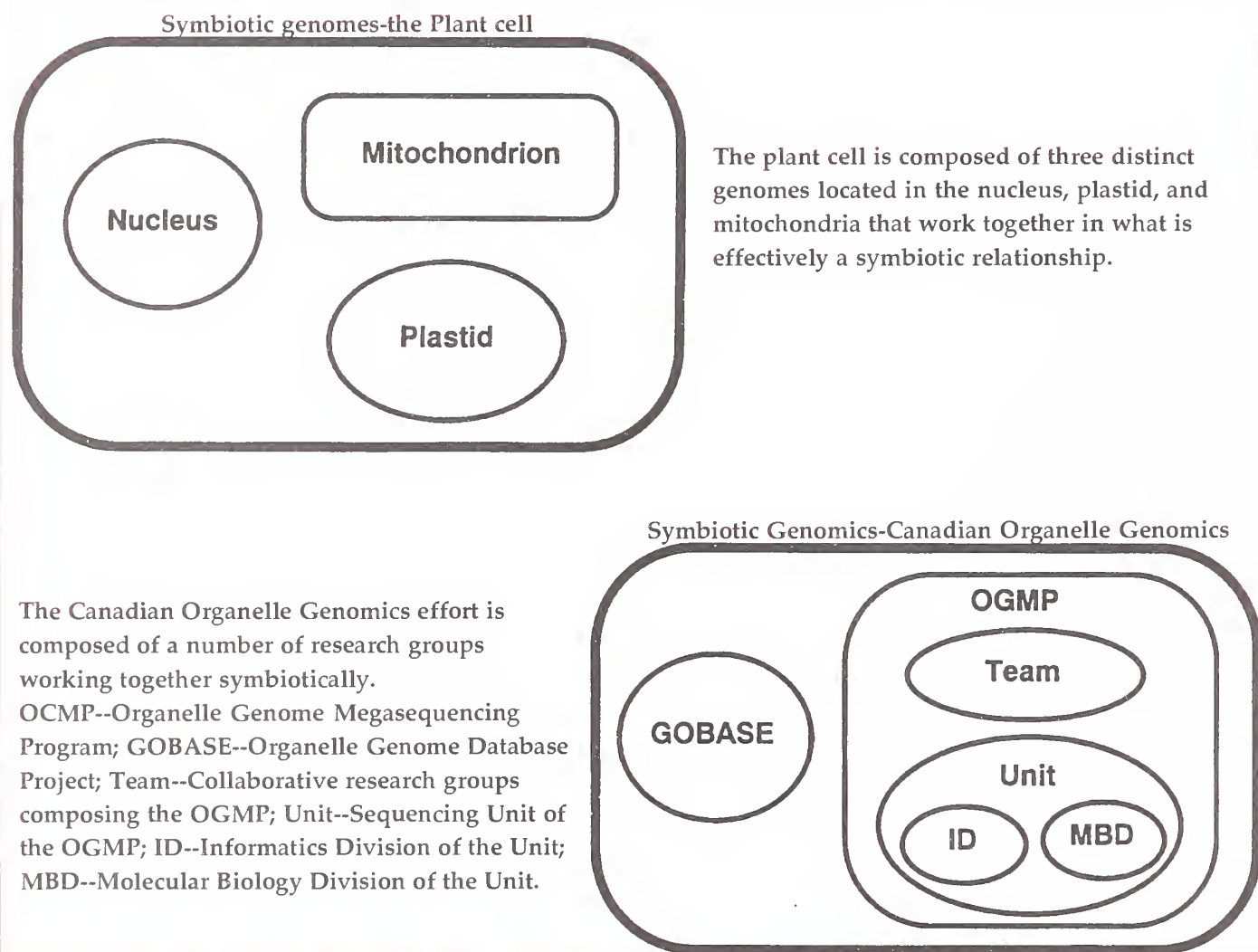
OGMP:

<http://megasun.bch.umontreal.ca/ogmp/ogmp.html>

GOBASE:

<http://megasun.bch.umontreal.ca/gobase/gobase.html> or by e-mail (table 1).

Figure 1. Organelle genomes and genomics



## Acknowledgments

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- Wolff, G., I. Plante, B.F. Lang and others. 1994. "Complete sequence of the mitochondrial DNA of the chlorophyte alga *Prototheca wickerhamii*. Gene content and genome organization." *Journal of Molecular Biology* 237:74-86.



## Introducing: Dr. David Grant



**D**r. David Grant is a USDA/ARS geneticist at Iowa State University, Ames, Iowa, and curator of the SoyBase database.

Grant joined ARS in 1995, after 12 years at Pioneer Hi-Bred International, in Johnston, Iowa. At Pioneer, he was project leader for the Molecular Genetics Project, where he developed and used molecular markers in plant breeding. His focus was on maize, though throughout his career he has also studied and published widely on *Neurospora* and *Chlamydomonas*.

Before joining Pioneer, Grant was an assistant research professor in the Department of Biochemistry, St. Louis University School of Medicine, where he was previously

a postdoctoral associate. Before his work in St. Louis, he was a postdoctoral fellow in the departments of Biology and Zoology at Duke University, Durham, North Carolina. He is a native of Houston, Texas.

As SoyBase curator, Grant, with the assistance of Marcia Imsande, maintains and updates the database and does presentations and training. He is also involved in making modifications to the database models, such as expansions to include new data types and changes to old models to facilitate their use. In the future, he plans to add new data types, such as graphical pedigrees, QTL maps, composite genetic maps, and others. "I hope SoyBase will evolve into an indispensable tool for soybean geneticists

and breeders," he says.

Grant encourages contributions from the soybean community. "SoyBase can only be as useful as the data it includes. If there is something that should be included or changed in the database, please let us know," Grant says. "In particular, we are interested in mapping information so we can include it in the composite genetic map. We can accept data in any format."

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## A Guide to Scientific Names of Vascular Plants

James L. Reveal  
Department of Plant Biology  
University of Maryland  
College Park, Maryland

I have always been amazed by biologists at the cutting edge of science who are so distressed that taxonomists—those who deal with the identification, naming, and classification of living things—might change the names of their favorite organisms or classify them differently from what they learned at the beginning of their careers. It is almost as if science should be allowed to progress in every realm except for systematic biology.

The development of new molecular techniques allowing the study of relationships in a fashion never before seen in biology is radically altering the classification of plants, particularly vascular plants—those generally referred to as the ferns, fern-allies, gymnosperms, and angiosperms. In addition, a detailed evaluation of the scientific names that I am conducting might cause some names in current use to be altered.

Scientific names of plants are governed by the *International Code of Botanical Nomenclature*, the provisions of which are managed by the International Association for Plant Taxonomy under the ultimate authority of the United Nations. Provisions in the *Code* are reviewed every 6 years, with the most recent

review having been held in 1993. The present *Code* contains provisions that should significantly reduce name changes solely for nomenclatural reasons. It is now possible to conserve names of species; conservation of names of

who have concentrated on arranging generic names into families (Brummitt 1992; Greuter et al. 1993; Gunn et al. 1992; Wielgorskaya 1995). Watson and Dallwitz (1991) have placed their family descriptions on the Internet, and they are updating the information from time to time.

To assist non-taxonomists in dealing with scientific names

### Developments

genera and families has long been possible. Furthermore, we can now reject any name that would cause nomenclatural instability. Disruption of widely used names should be a thing of the past.

Nonetheless, relatively few names are changed for nomenclatural reasons. Most are altered, in fact or in concept, as a result of evidence from new research that shows a previous disposition to be incorrect. Taxonomic changes are made only to accommodate new evidence; such changes may or may not affect nomenclature. The *Code* does not regulate taxonomic judgment, only nomenclature.

In recent years, several workers have proposed new, broad systems of classification for higher plants. These works (Dahlgren 1989a, b; Cronquist 1981, 1988; Takhtajan 1986, 1987; Thorne 1992a, b) have been augmented by others

above the rank of genus, the *Indices Nominum Supragenericorum Plantarum Vascularium* Project, sponsored by the International Association for Plant Taxonomy and the Norton-Brown Herbarium at the University of Maryland at College Park, in cooperation with the National Agricultural Library at Beltsville, Maryland, is providing a series of interactive databases that offer the following:

(1) An index to all validly published names for vascular plants proposed above the rank of genus. Each name is provided with a full bibliographic citation.

(2) A concordance of how each of the authors cited above, including myself, treat each family name. In this way, it is possible to ascertain the disposition of any validly published family name.

(3) A linear sequence, either alphabetical or phylogenetic, of all of the families' names recognized by

each author, as well as each family's synonymy.

(4) A listing of the full phylogenetic arrangement of the flowering plants from the rank of division to family accepted by Cronquist, Dahlgren, and Thorne. The new but yet-to-be-published system of Takhtajan will be added in the near future. Also available shortly will be a full phylogenetic arrangement of all extant vascular plants that I accept.

The *Indices* can be accessed at: [http://www.inform.umd.edu:8080/EdRes/Colleges/LFSC/life\\_sciences/.plant\\_biology/.WWW/supragen.html](http://www.inform.umd.edu:8080/EdRes/Colleges/LFSC/life_sciences/.plant_biology/.WWW/supragen.html)

The *Indices* also provide direct access to the descriptions given by Watson and Dallwitz, and to the dispositions of the genera according to the U.S. Department of Agriculture, edited by John Wiersema. A splitter's guide to the flowering plants was recently published (Reveal 1993). At present, the detailed survey of the botanical literature has concentrated on works published before 1860. In time, all suprageneric names should be included in the *Indices*.

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## World Wide Web



USDA, ARS  
National Agricultural  
Library

Plant GENOME Data & Information Center

[pgenome@nal.usda.gov](mailto:pgenome@nal.usda.gov)

Our URL Address is: <http://www.nal.usda.gov/pgdic/>

The Plant Genome Data and Information Center (PGDIC) provides access to a variety of information products and services on all aspects of plant and animal genome mapping.

## Hard Copy



# Biosafety Proceedings Available From PGDIC; Japan Selected for Fourth Symposium

The proceedings containing 60 scientific papers presented at the Third Annual Symposium on the Biosafety Results of Field Tests of Genetically Modified Plants and Microorganisms, held November 13-16, 1994, in Monterey, California, are now available from the Plant Genome Data and Information Center.

The proceedings present discussions of hard-hitting issues pertaining to recombinant DNA technology, with a focus on sophisticated safety data obtained after years of research in small- and large-scale field tests. The symposium's 225 participants represented 34 countries, many of which were developing nations just beginning to enter the biotechnology arena.

A highlight of the symposium was the remarks by luncheon speaker Ding Yong, deputy director at the China National Center for Biotechnology Development in Beijing. Yong discussed his government's 1993 implementation of the 7th Command, which regulates biotechnology research and industrial and agricultural activities in China based on four levels of safety. This regulation includes provisions that carefully weigh the human and environmental impact of field-testing biotech plants and microorganisms. Some products currently under investigation include

tomatoes, potatoes, corn, and cotton. In addition, Yong said China is willing to share its biosafety data with other nations.

Other speakers described the results of field-testing virus-resistant squash in the United States and Mexico; field assessments of papaya, cucurbits, tomatoes, rhizobia, tobacco mosaic virus, potatoes, and flax; encapsidation (combining parts) of viruses in transgenic plants; gene escape in transgenic sugar beet; the biosafety results of transgenic rice plants in Japan; and allergenicity issues.

Evening workshops focused on databases for biosafety, public information and consumers' perspectives, and new risk assessment paradigms.

The symposium was sponsored by USDA; the European Commission; the Society for Techno-Innovation in Agriculture, Fisheries, and Forestry in Japan; EPA; Clemson University; and the University of California-Davis. To obtain a copy, please contact PGDIC, NAL, ARS, USDA, 10301 Baltimore Ave., Beltsville, MD 20705-2351; phone: (301) 504-6613; fax: (301) 504-7098; e-mail: [pgenome@nal.usda.gov](mailto:pgenome@nal.usda.gov)

The fourth biosafety symposium will take place in Tsukuba Science City, Japan, July 14-18, 1996, according to Alvin Young, science adviser for CSREES and co-organizer

of three preceding symposia.

The meeting will center on six panels that will address such issues as agronomic products in the marketplace; emerging capabilities of developing countries; risk assessment; field experience using microorganisms as bioindicators, biosensors, or biomonitors; new research techniques for biosafety evaluations; and international cooperation.

The host institution will be the Japan International Research Center for Agricultural Science. Keiji Kainuma, Director General of the Center, will chair the meeting. For more information, please write to Akihiro Hino, Deputy Director, Biotechnology Division, Ministry of Agriculture, Forestry and Fisheries, 1-2-1 Kasumigaseki, Chiyoda, Tokyo 100 Japan; or call +81-3-3502-3919; FAX: +81-3-3502-4028; E-mail: [akhino@s.affrc.go.jp](mailto:akhino@s.affrc.go.jp) ♦

## Andrew Kalinski

1947 - 1995

Following the death of Andrew Kalinski last fall, requests for information addressed to him have been and will continue to be handled by other PGDIC staff members.

## Off the Wire



# Germplasm Resources on the Internet

*Organisms and Strains* is an annotated guide to germplasm resources on the Internet. It is divided into three sections: animal stock centers, plant stock centers, and microorganisms and fungi. The guide is maintained through the efforts of Indiana University and the University of Wisconsin.

Plant germplasm repositories or databases listed as of January 11, 1996 include: Agricultural Genome Databases (AGIS), American Type Culture Collection, *Arabidopsis* sources (*Arabidopsis* Information Management System (AIMS), Lehle Seeds, and Nottingham *Arabidopsis* Stock Centre), Center for Genetic Resources (Netherlands), Culture Collection of Algae and Protozoa

(U.K.), DSM—the German Collection of Microorganisms and Cell Cultures, Forest Genetic Resources in Germany, Geilweilerhof International Grapevine Database, International Bambara Groundnut Database, Germplasm Resource Information Network (GRIN), Index Seminum Austriae, Maize Genetics Corporation Stock Center, National Clonal Germplasm Repository, Nordic Gene Bank, the University of Texas at Austin Algae Culture Collection, and the Vavilov Institute.

David Jourdan, of Steenbock Library and the Biotechnology Center, University of Wisconsin, Madison, compiles the guide. He hopes to focus more heavily on

plants in the future, adding, "I think that in the very near future many germplasm repositories will have their catalogs on the Internet, and having an annotated guide to these resources will be useful in informing researchers of what's available."

The guide can be found on the World Wide Web at:

<http://biotech.chem.indiana.edu/pages/orgstrain.html>

To submit new resources or suggest changes, please contact:

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Fax: (608) 263-3221

E-mail: [djourdan@macc.wisc.edu](mailto:djourdan@macc.wisc.edu) ♦

## NAL Catalog on Internet

ISIS, the Online Public Access Catalog (OPAC) of the National Agricultural Library (NAL), is now available over the Internet at telnet address: [opac.nal.usda.gov](http://opac.nal.usda.gov). The catalog can be searched Monday through Saturday from 6 a.m. to 9 p.m., Eastern Standard Time.

According to NAL Director Pamela André, while this improvement will help all users of the Library, it will be of particular interest to those who are outside the Washington, D.C. area. "Over the years, NAL has become an internationally recognized resource for the agricultural community, serving thousands of scientists, researchers, and scholars throughout the world.

To have Internet access to these resources will help to meet a critical need for agricultural information worldwide," says André.

ISIS contains *two* agricultural databases, the NAL Online Catalog and the Journal Article Citation database. The NAL Online Catalog is updated by NAL and contains the most current bibliographic citations for books, reports, maps, periodicals, audiovisuals, CD-ROM's and other materials being added to the NAL collection. It also includes citations for materials at the U.S. Reference Center and five Regional Research Center Libraries of USDA's Agricultural Research Service.

The Journal Article Citation database consists of citations of journal and periodical articles, book chapters, reprints, and other specialized materials indexed by NAL and its cooperators. It is part of NAL's AGRICOLA database, which contains over 3 million agriculture-related citations.

For more information, please contact John Stetka, Information Systems Division, Room 013, National Agricultural Library, USDA, ARS, 10301 Baltimore Ave., Beltsville, MD 20705-2351; phone: 301-504-6816; TDD/TTY: 301-504-6856; Fax: 301-504-7473; E-mail: [jstetka@nal.usda.gov](mailto:jstetka@nal.usda.gov) ♦

## On the Horizon



# Calendar of Upcoming Events

## MEETINGS/WORKSHOPS

October 6-10, 1996: **American Society for Horticultural Science Annual Meeting**, Lexington, KY. VOICE: (703) 836-4606.

October 17-20, 1996: **Fourth McGill University Conference on Regulation of Eukaryotic DNA Replication**, St. Sauveur, Quebec, CN. Contact: WWW: <http://www.mcgill.ca/mcgill/servers/Admin/UBO/dna.html>

October 20-24, 1996: **Genetics and Molecular Biology of Industrial Microorganisms**, Bloomington, IN. Contact: SIM, 3929 Old Lee Hwy., Suite 92A, Fairfax, VA 22030-2421. VOICE: (703) 691-3357, FAX: (703) 691-7991.

October 20-25, 1996: **Recovery of Biological Products VIII**, Tucson, AZ. Contact: American Chemical Society, Meetings Dept., 1155 16th St., NW, Washington, DC 22036. VOICE: (202) 872-6286, FAX: (202) 872-6128, E-MAIL: [a\\_aguzin@acs.org](mailto:a_aguzin@acs.org)

November 3-8, 1996: **Annual Meeting American Society of Agronomy**, Indianapolis, IN. Contact: American Society of Agronomy, 677 South Segoe Rd, Madison, WI 53711. VOICE: (608) 273-8080, FAX: (608) 273-2021.

November 21-22, 1996: **European Biotechnology Symposium, Congress Centrum**, Cologne, Germany. Contact: BioConferences International, 4405 East-West Highway, #501, Bethesda, MD 20814. FAX: (301) 652-3072.

December 7-11, 1996: **6th International Congress on Cell Biology and the 36th American Society for Cell Biology Annual Meeting**, San Francisco, CA. Contact: American Society for Cell Biology, 9650 Rockville Pike, Bethesda, MD 20814-3992. VOICE: (301) 530-7153, FAX: (301) 530-7139, E-MAIL: [congress@ascb.faseb.org](mailto:congress@ascb.faseb.org)

January 12-16, 1997: **Plant and Animal Genome V, Town and Country Hotel**, San Diego, CA. Contact: Scherago International, Inc., 11 Penn Plaza, Suite 1003, New York, NY 10001. VOICE: (212) 643-1750, FAX: (212) 643-1758, E-MAIL: [pag5@scherago.com](mailto:pag5@scherago.com)

January 16-18, 1997: **Annual Symposium in Plant Physiology: A Look Beyond Transcription: Mechanisms Determining RNA Stability and Translation in Plants**, University of California, Riverside, CA. Contact: Cindi McKernan, Botany

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<http://www.nal.usda.gov/pgdic>

*Our calendar of events is updated on a monthly basis.*

and Plant Sciences Dept., University of California, Riverside, CA 92521. VOICE: (909) 787-3423, FAX: (909) 787-4437, E-MAIL: cindi.mckernan@mail.ucr.edu

January 20-26, 1997: **Keystone Symposia on Molecular and Cellular Biology: Evolution of Plant Development, Taos, NM.** Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. VOICE: (800) 253-0685, FAX: (970) 262-1525; E-MAIL: keystone@symposia.com, WWW: <http://www.colorado.net/symposia>

February 1-6, 1997: **Keystone Symposia on Molecular and Cellular Biology: RNA-Protein Interactions, Taos, NM.** Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. VOICE: (800) 253-0685, FAX: (970) 262-1525; E-MAIL: keystone@symposia.com, WWW: <http://www.colorado.net/symposia>

February 6-11, 1997: **Keystone Symposia on Molecular and Cellular Biology: Frontiers of NMR in Molecular Biology, Taos, NM.** Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. VOICE: (800) 253-0685, FAX: (970) 262-1525; E-MAIL: keystone@symposia.com, WWW: <http://www.colorado.net/symposia>

February 16-21, 1997: **Keystone Symposia on Molecular and Cellular Biology: Molecular Mechanisms of Evolution: Structure, Function, Expression and Regulation of Genes and Proteins, Santa Fe, NM.** Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. VOICE: (800) 253-0685, FAX: (970) 262-1525; E-MAIL: keystone@symposia.com, WWW: <http://www.colorado.net/symposia>

March 1-7, 1997: **Keystone Symposia on Molecular and Cellular Biology: Transposition and Site-**

**Specific Recombination, Santa Fe, NM.** Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. VOICE: (800) 253-0685, FAX: (970) 262-1525; E-MAIL: keystone@symposia.com, WWW: <http://www.colorado.net/symposia>

March 3-9, 1997: **Keystone Symposia on Molecular and Cellular Biology: Protein Folding, Modification and Transport in the Early Secretory Pathway, Taos, NM.** Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. VOICE: (800) 253-0685, FAX: (970) 262-1525, E-MAIL: keystone@symposia.com, WWW: <http://www.colorado.net/symposia>

April 6-11, 1997: **Keystone Symposia on Molecular and Cellular Biology: Metabolic Engineering in Transgenic Plants, Copper Mountain, CO.** Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. VOICE: (800) 253-0685, FAX: (970) 262-1525; E-MAIL: keystone@symposia.com, WWW: <http://www.colorado.net/symposia>

April 14-19, 1997: **9th International Congress on Isozymes, Genes, and Gene Families, San Antonio, TX.** Contact: Daphne Wright, Congress Liaison, Southwest Foundation for Biomedical Research, P.O. Box 28147, San Antonio, TX 78228-0147. FAX: (210) 670-3337, E-MAIL: isozyme@darwin.sfbr.org

May 29-June 1, 1997: **International Symposium in Root Biology--Radicle Molecules: The Biology of Underground Plant Metabolism, University Park, PA.** Contact: Dr. Hector E. Flores, Pennsylvania State University, 315 Wartik Laboratory, University Park, PA 16802. VOICE: (814) 865-2955, FAX: (814) 863-7217, E-MAIL: hector\_flores@agcs.psu.edu

June 8-12, 1997: **BIO '97: International Biotechnology Meeting and Exhibition, Houston, TX.** Contact: BIO International Meetings Dept., Biotechnology Industry Organization, 1625 K St., NW, Suite 1100, Washington, DC 20006-1604. VOICE: (202) 857-0244, FAX: (202) 331-8132 or (202) 857-0237.

June 8-19, 1997: **XVIII International Grassland Congress, Winnipeg, CN.** Contact: XVIII International Grassland Congress, P.O. Box 4520, Station C, Calgary, Alberta, Canada T2T 5N3. VOICE: (403) 244-4487, FAX: (403) 244-2340, E-MAIL: amc@supernet.ab.ca, WWW: <http://www.forage.com>

June 26-30, 1997: **Eighth International Conference on Arabidopsis Research, Madison, WI.** Contact: Rick Amasino. E-MAIL: amasino@biochem.wisc.edu

August 2-6, 1997: **Annual Meeting American Society of Plant Physiologists, Vancouver, British Columbia, CN.** Contact: Program Committee, c/o ASPP Headquarters, 15501 Monona Dr., Rockville, MD 20855-2768. VOICE: (301) 251-0560, FAX: (301) 279-2996, E-MAIL: chambers@aspp.org

August 13-15, 1997: **Symposium on Seed Biology and Technology: Applications and Advances, National Seed Storage Laboratory, Fort Collins, CO.** Contact: Eric E. Roos, USDA National Seed Storage Laboratory, 1111 South Mason St., Fort Collins, CO 80521-4500, VOICE: (970) 495-3205, FAX: (970) 221-1427, E-MAIL: eroos@lamar.colostate.edu, WWW: <http://www.ars-grin.gov/ars/NoPlains/FtCollins/SEEDBIO/>

August 24-29, 1997: **17th International Congress of Biochemistry and Molecular Biology (in conjunction with) 1997 Annual Meeting of the American Society for Biochemistry and Molecular Biology, San Francisco, CA.** Contact: Congress Secretariat, 17th International Congress for Biochemistry and Molecular Biology, 9650 Rockville Pike, Bethesda, MD 20814-3996. FAX: (301) 571-1824, E-MAIL: 171UBMB@asbmb.faseb.org

September 21-27, 1997: **5th International Congress of Plant Molecular Biology, Singapore.** Contact: Congress Secretary, Department of Biochemistry & Molecular Biology, University of Georgia, Athens, GA 30602-7229. FAX: (706) 542-2090

October 23-30, 1997: **Annual Meeting American Society of Agronomy, Anaheim, CA.** Contact: American Society of Agronomy, 677 South Segoe Rd, Madison, WI 53711. VOICE: (608) 273-8080, FAX: (608) 273-2021.

July 1998: **4th Asia Pacific Conference on Agricultural Biotechnology, Darwin, Australia.** Contact: Dr. Phil Larkin, CSIRO, Division of Plant Industry, P.O. Box 1600 Canberra, A.C.T. 2601, Australia. VOICE: +61 6 2465060, FAX: +61 6 2465000, E-MAIL: p.larkin@pi.csiro.au

October 18-22, 1998: **Annual Meeting American Society of Agronomy, Baltimore, MD.** Contact: American Society of Agronomy, 677 South Segoe Rd, Madison, WI 53711. VOICE: (608) 273-8080, FAX: (608) 273-2021.

October 30-November 4, 1999: **Annual Meeting American Society of Agronomy, Salt Lake City, UT.** Contact: American Society of Agronomy, 677 South Segoe Rd, Madison, WI 53711. VOICE: (608) 273-8080, FAX: (608) 273-2021.

**APSKarnal Bunt On-Line Symposium:** Sponsored by The American Phytopathological Society.  
URL: <http://www.scisoc.org/karnal.htm>

Information Center, 10301 Baltimore Ave., 4th Flr., Beltsville, MD 20705-2351. VOICE: (301) 504-6613, FAX: (301) 504-7098, E-MAIL: [pgenome@nal.usda.gov](mailto:pgenome@nal.usda.gov)

## TRAINING/COURSES

September 30-October 4, 1996: **RNA Isolation and Gene Expression, Columbia, MD.** Contact: Workshop Coordinator, Exon-Intron, Inc., 9151 Rumsey Rd., Suite 130, Columbia, MD 21045. VOICE: (800) 407-6546, FAX: (410) 730-3983.

October 10-23, 1996: **YACs in Structural and Biological Genome Analysis, Cold Spring Harbor, NY.** Contact: Cold Spring Harbor Laboratory. VOICE: (516) 367-8346, FAX: (516) 367-8845, E-MAIL: [meetings@cshl.org](mailto:meetings@cshl.org), WWW: <http://www.cshl.org>

December 3-4, 1996: **Molecular Biology E-mail Servers Training Program, Beltsville, MD.** Contact: Evelyn Jones, USDA, ARS, National Agricultural Library, Plant Genome Data and

## RESEARCH FELLOWSHIPS AND GRANTS

**Undergraduate Summer Research Fellowships in Root Biology.** Contact: Dr. Hector E. Flores, Pennsylvania State University, 315 Wartik Laboratory, University Park, PA 16802. VOICE: (814) 865-2955, FAX: (814) 863-7217, E-MAIL: [hector\\_flores@agcs.psu.edu](mailto:hector_flores@agcs.psu.edu)

**NSF-Sponsored Graduate Research Traineeships in Plant Biology.** Contact: Dr. Elizabeth Bray, Dept. of Botany and Plant Sciences, University of California, Riverside, CA 92521. VOICE: (909) 787-4548, FAX: (909) 787-4437, E-MAIL: [bray@mail.ucr.edu](mailto:bray@mail.ucr.edu) ♦

## Taking Stock



# Stock Center Profile: The C.M. Rick Tomato Genetic Resources Center

The C.M. Rick Tomato Genetic Resources Center (TGRC), located at the University of California, Davis, is a genebank of wild relatives, monogenic mutants, and miscellaneous genetic stocks of tomato. It is currently curated by Dr. Roger T. Chetelat in the Department of Vegetable Crops.

The genebank was founded by Dr. Charles Rick, who collected many of the wild species accessions in South



America and whose research program produced many of the marker and cytogenetic stocks. Before its establishment, stocks were shared informally under the auspices of the Tomato Genetics Cooperative (TGC), a group of tomato researchers interested in genetics, linkage, mapping, and breeding. Rick served as publisher of the TGC's annual report, which in-

cluded lists of available stocks and their sources. In 1976, Rick received a National Science Foundation grant to support maintenance of the collection, then named the Tomato Genetic Stocks Center. It was renamed in 1990 to honor Rick's contributions and indicate that it contains resources beyond stocks.

Researchers at the TGRC and worldwide continue to collect wild species and construct new genetic stocks. In recent years, the collection has grown by about 100-200 items per year.

The TGRC currently houses 1,059 accessions of wild species, which include representatives of all nine *Lycopersicon* species, as well as four related *Solanum* species. Monogenic mutants (963 accessions) include spontaneous and induced mutations affecting all aspects of plant development, introgressed disease resistance genes, and protein marker stocks. Miscellaneous genetic stocks (1,187 accessions) include linkage tester stocks, trisomics, translocations, Latin American varieties, and various types of interspecific prebreds.

New genetic stocks include collections of monogenic mutants nearly isogenic in uniform genetic backgrounds, a library of introgressed alien chromosome segments, and dominant resistance genes for emerging diseases. In the future, TGRC researchers hope to incorporate transgenic germplasm, such as antisense and transposon insertion mutants.

Seed samples are distributed free to researchers worldwide, for a wide variety of research projects. A major area of activity is the use of wild germplasm for disease resistance, with new useful resistances being reported each year. Researchers have discovered resistance to at least 42 major diseases in exotics and

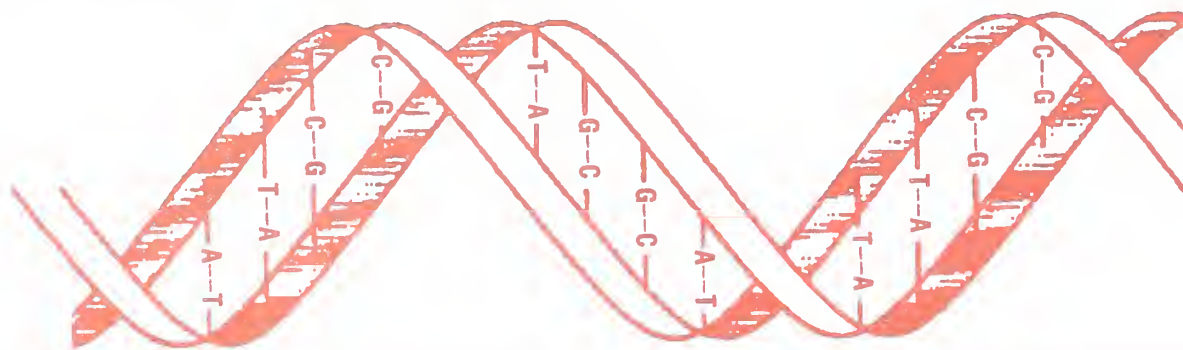
have bred 20 of them into horticultural tomatoes. Other traits of economic interest include insect resistance, abiotic stress tolerance, and improved horticultural and fruit characteristics. TGRC stocks are also cited frequently in studies of tomato physiology and development, genetics, and molecular genetics.

TGRC researchers conduct ongoing projects in several areas. Currently, they are using molecular marker techniques to identify chromosome segments of two previously inaccessible *Solanum* species introgressed into a tomato background.

Researchers also maintain a computer database, which includes passport information on all accessions, with detailed collection notes for wild species, a list of the known mutants of tomato, records of seed requests, and a growing library of digital images for tomato stocks. Information is periodically uploaded to the genome database SolGenes. Stock lists are also available electronically (e-mail: [tgrc@vegmail.ucdavis.edu](mailto:tgrc@vegmail.ucdavis.edu)) and are published annually in the Tomato Genetics Cooperative Report.

For further information, contact:

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Department of Vegetable Crops  
University of California  
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Phone: (916) 752-6726  
Fax: (916) 752-9659  
E-mail: [chetelat@vegmail.ucdavis.edu](mailto:chetelat@vegmail.ucdavis.edu) ♦



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## Using Fuzzy Searching To Retrieve Plant Genome Information at the USDA, National Agricultural Library

Douglas W. Bigwood  
Manager, Genome Informatics Group  
Information Systems Division  
USDA, ARS, National Agricultural Library  
Beltsville, MD

One of the difficulties in searching any data resource is the lack of a facility to find items that are close to, but not exactly like, the search terms(s) of interest. Wildcarding (for example: the use of asterisks in some search software) aids the user to a certain degree, but often the results re-

turned are not exactly what is desired. A fuzzy searching facility, using a program called agrep, is provided on the Agricultural Genome World Wide Web Server at the National Agricultural Library. A brief description of how to use this facility, along with some hints and examples, follows.

To connect with the agrep search form, open the following

URL in your World Wide Web browser:  
<http://probe.nal.usda.gov:8300/agrepquery.html>

You will be presented with a form similar to that shown in figure 1.

The form allows you to select three search parameters: case-sensitivity (default is case-insensitive), whether to search for the pattern as a "word" (as opposed to the pattern occurring as a part of a word; default is to search for pattern as a word),

and whether or not to search for the pattern as a superset (for example: "the only" matches "the one and only"; default is do not search for pattern as a superset). You may also select zero, one, or two mismatches. A mismatch may be an insertion (for example: "Lansberg" will match "Landsberg"), a deletion ("adh-1" will match adh1), or a substitution ("Smith" will match "Smyth"). A cautionary note: allowing two mismatches can result in a slew of unexpected results, particularly if one short search term is used. For example, searching for the pattern "adh" with two mismatches will bring back any object containing an a, d, or h.

One simple but common use for agrep is to account for differences in the British and American spellings of various words such as center/centre and color/colour. Other common usages include searching for a person's name you do not know how to spell and adjusting to slight differences in gene nomenclature among taxa.

Search terms can be combined to perform boolean searches using a terse notation: "this,that" translates to "this or that"; "here,there" translates to "here and there." The

Figure 1. The agrep query form  
agrep search options:

Fill in search string, pick options, then

[Return to the list of articles](#)

[Go to help with agrep](#)

---

Search for: smith locus

Use # as a wildcard, e.g. h#e matches bella

Booleans: use a comma for OR and a semicolon for AND

- ☐ Case-insensitive search
- ☐ Search for the pattern as a word i.e., surrounded by spaces, tabs, or other non-alphanumeric characters
- ☐ Search for the pattern as a superset, e.g., the pattern "the only" matches "the one and only"

Allow mismatches (insertions, deletions, substitutions):

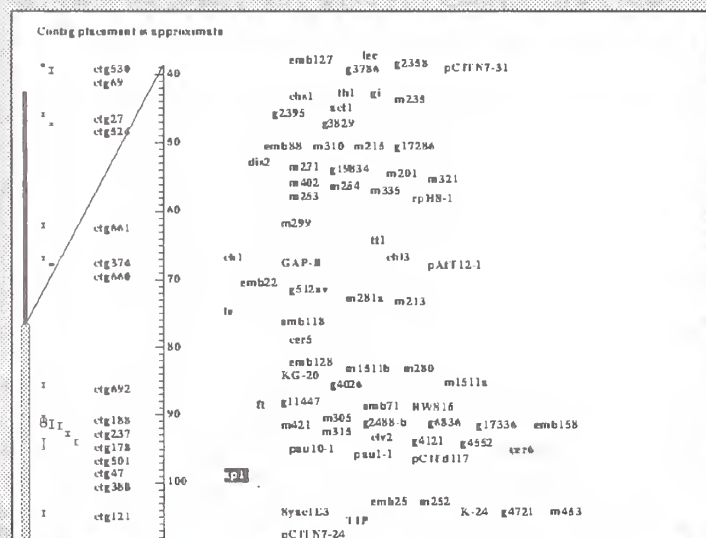
zero ☒ one ☐ two ☐

Search the following databases: ☐ All

- ☒ All Plants
  - ☐ SoyBase (Soybeans)
  - ☐ AARD (Arabidopsis)
  - ☐ MolGenes (Solanaceae)
  - ☐ TreeGenes (forest trees)
  - ☐ ChlamyDB (Chlamydomonas)
  - ☐ All Grasses

- Paper: hines-1993-ahga
- Paper: hines-1993-ahga
- Paper: bowman-1989-asdrk
- Paper: wise-1992-aslyc
- Paper: alvar-1992-asrba
- Paper: smith-1995-aari
- Genre Class: crc
- Genre Class: crc
- Genre Class: spd
- Genre Class: ut
- locus: ori
- locus: as
- locus: mp7
- locus: crc
- locus: pld

**7** or more information on this or other search tools, please refer to the article, "Simple Search Tools Can Save Time," Probe, Volume 4, Number 3/4, pages 19-20 which can be found on PGDIC's homepage:



## SGML—Enhances Access to Digital Information

*Susan McCarthy, Coordinator  
Plant Genome Data and Information Center  
USDA, ARS, National Agricultural Library  
Beltsville, MD*

Imagine being able to connect to the greatest archive of agricultural information from anywhere in the world 24 hours a day. Once connected, you search through the entire collection using key concepts. When the search is completed, you have a custom-tailored, synthesized document that retains source attributions but contains only the relevant pieces of the entire collection.

This scenario is still a dream, although we are closer to achieving it than ever before. Underlying this dream is Standard Generalized Markup Language (SGML). "Standard" and "Generalized" are the two key concepts. A standard allows searching across many different sources while providing the capacity to reconstitute the results in a common format. A generalized standard can adapt to many different formats and unique situations.

Markup languages help authors and publishers organize their work by structuring the content. The structure has a strong display component that helps the reader to understand the author's meaning. We all use markup

language whenever we use punctuation, spacing—both horizontal and vertical—font selection, and the like.

The SGML mark-up language identifies key concepts for document content (for example: introduction, references, paragraphs) and display elements through a standard document type definition (DTD), and style sheets.

Our dream must again be anchored on the "standard" ideal to allow independence of hardware and software platforms. This standard should be internationally recognized to extend access to materials over time despite the rapid technological changes. Such recognition for ASCII has exploded the boundaries of telecommunication.

Today, we are beginning to build an experimental digital core based on SGML here at the USDA's National Agricultural Library. A collaboration has been forged with the Bean Improvement Cooperative to digitize its complete series of annual reports and conference proceedings.

This experiment will achieve its greatest success only with the full participation of NAL users. Accu-

rately identifying and defining the keyword/keyphrase concepts is the only means to guarantee that users will be able to search and retrieve appropriate text across the entire body of knowledge.

To begin, we have placed sample articles on our homepage (<http://www.nal.usda.gov/pgdic>), and we invite everyone to take a look at the "digital core." You are cordially invited to participate in our experiment. Just remember: your participation at the ground floor may influence how *you* access information in the not-so-distant future. ♦



## Transitions

Susan McCarthy, Coordinator  
Plant Genome Data and Information Center  
USDA, ARS, National Agricultural Library  
Beltsville, MD

Communication links all living organism--from unconscious chemical signals to abstract written concepts. Human communication has changed remarkably in the last 5 years. The latest communication revolution is rooted in the global network called the Internet. We are just at the beginning of this revolution.

An earlier communication revolution was catalyzed by the development of movable type and the printing press. Profound cultural and social changes arose. The Internet may well bring equally profound changes in our time.

Ironically, change is one of the few constants in life. Closing the doors on *Probe* is a bittersweet transition for the staff of the Plant Genome Data and Information Center. You have been a wonderful audience providing valuable ideas and kind support. Although the newsletter will cease publication, we hope that many of you will remain in contact with us through our listserv.

I would like to take this opportunity to thank the many people who helped make *Probe* a success. Foremost, I would like to thank Dr. Jerome Miksche for giving us this splendid forum. Terry Henrichs has been the creative force in designing and producing each issue from start to finish. JoAnne Meil, Caroline Bigwood, and Marti Asner have provided expert editorial services, a matter of great value to me since my high school teacher assured me that sentence fragments and dangling participles would be the death of me (Mrs. Shanks, you were so right!). Barbara Buchanan scans many sources each month to create an up-to-date and useful resource, the calendar of events. Our graduate students, Annette Colbert, Ed Donald, and Judy Ruttenberg managed the mailing list and distributed requested publications. Ultimately, our authors contributed many high-caliber, timely articles that were so essential to *Probe's* success. My sincerest thanks to all.

While we are closing the door on *Probe*, we will open a new door to the world of Internet. Please visit us frequently at <http://www.nal.usda.gov/pgdic>. ♦

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